

Claims

- [c1] 1.A method for identifying a transcribed genomic region comprising:
providing a nucleic acid sample comprising transcripts or nucleic acids derived from transcripts from the genome;
hybridizing the nucleic acid sample with a plurality of nucleic acid probes, wherein the probes are designed to interrogate potential transcripts from both strands of the genomic DNA;
analyzing hybridization signals to detect the transcribed region.
- [c2] 2.The method of claim 1 where the plurality of probes comprises probes interrogating the intergenic, and intronic regions of the genome.
- [c3] 3.The method of Claim 2 wherein the plurality of nucleic acid probes are immobilized on a substrate at a density greater than 400 different probes per cm^2 .
- [c4] 4.The method of Claim 3 wherein the plurality of nucleic acid probes are immobilized on a substrate at a density greater than 1000 different probes per cm^2 .
- [c5] 5.A method for detecting an operon element in a prokaryote organism comprising;
hybridizing transcripts or nucleic acids derived from transcripts from the organism with a plurality of probes, wherein the probes interrogate transcription of an intergenic region between two flanking open reading frames (ORFs); and
classifying the intergenic region as a potential operon element if both flanking ORFs are expressed and if the intergenic region is transcribed off the same DNA strand as the flanking ORFs.
- [c6] 6.The method of Claim 5 wherein the probes are oligonucleotides immobilized on a substrate.
- [c7] 7.The method of Claim 6 wherein the probes are immobilized at a density of at least 400 different probes per cm^2 .

- [c8] 8.The method of Claim 7 wherein the plurality of nucleic acid probes are immobilized on on a substrate at a density greater than 1000 different probes per cm².
- [c9] 9.The method of Claim 8 wherein classifying the intergenic region as operon element if both flanking ORFs are expressed and if the intergenic region is transcribed off the same DNA strand as the flanking ORFs and if transcription in the intergenic region is detected by more than 60% of the probes targeting the intergenic region.
- [c10] 10.The method of Claim 9 wherein the intergenic region is detected by more than 80% of the probes targeting the intergenic region.
- [c11] 11.The method of Claim 9 wherein the classifying comprises classifying the intergenic region as a potential operon element if both flanking ORFs are expressed and if the intergenic region is transcribed off the same DNA strand as the flanking ORFs and the transcription of the intergenic region is correlated with the transcription of at least one of the flanking ORFs.
- [c12] 12.The method of Claim 11 wherein the transcription of the intergenic region is correlated with the transcription of both flanking ORFs.
- [c13] 13. A method for detecting a 5' UTR for a gene comprising;
hybridizing a sample comprising transcripts or nucleic acids dervied from transcripts with a plurality of probes, wherein the probes interrogate transcription of an intergenic region immediately upstream the gene; and classifying the intergenic region as a potential 5'UTR of the gene if the intergenic region is transcribed in the same orientation of the gene and the trancribed region is greater than 70 bases in length.
- [c14] 14.The method of Claim 13 wherein the probes are oligonucleotides immobilized on a substrate.
- [c15] 15.The method of Claim 14 wherein the probes are immobilized at a density of at least 400 different probes per cm².
- [c16] 16.The method of Claim 15 wherein the plurality of nucleic acid probes are

immobilized on on a substrate at a density greater than 1000 different probes per cm².

[c17] 17. A method for detecting a 3' UTR for a gene comprising; hybridizing a sample comprising transcripts or nucleic acids dervied from transcripts with a plurality of probes, wherein the probes interrogate transcription of an intergenic region immediately down stream the gene; and classifying the intergenic region as a potential 3'UTR of the gene if the intergenic region is transcribed in the same orientation of the gene and the trancribed region is greater than 70 bases in length.

[c18] 18.The method of Claim 17 wherein the probes are oligonucleotides immobilized on a substrate.

[c19] 19.The method of Claim 18 wherein the probes are immobilized at a density of at least 400 different probes per cm².

[c20] 20.The method of Claim 19 wherein the plurality of nucleic acid probes are immobilized on on a substrate at a density greater than 1000 different probes per cm².